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Result
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ALIGNMENTS

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alpha-globulin type B precursor (tandem 1) - upland cotton (frag N;Alternate names: seed storage protein C;Species: Gossypium hirsutum (upland cotton) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change C;Accession: S08059 R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: glycinin
C;Keywords: glycoprotein; seed; storage protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-588/Product: alpha-globulin storage proprotein #status predicted <MAT>
F;417/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 1-81 <CH2>
C; Comment: This is a seed storage protein.
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A;Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII A;Reference number: A30838
A;Accession: A30838
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A; Accession: S06911
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A; Residues: 1-588 <CHI
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nes 39; Conserv
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1; Mismatches
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A; Reference number:

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A:Introns: 211/1; 269/3; 296/3; 391/3; 502/1
C:Superfamily: glycinin
C:Keywords: seed; storage protein
F:1-24/Domain: signal sequence #status predi
F:25-566/Product: vicilin #status predicted
                                                                                                                                              A;Cross-references:
C;Genetics:
                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-452 <MC2>
                                                                                                                                                                                                                                           R;McHenry, L.; Fritz, P.J.

Plant Mol. Biol. 18, 1173-1176, 1992

A;Title: Comparison of the structure and nucleotide sequence of vicilin genes of cocoa A;Reference number: S22477; MUID:92288309

A;Accession: S22477
                                                                                                                                                                                                          A;Cross-references:
A;Accession: S22478
                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-566 <MCH>
                                                                                                                                                                                                                                                                                                                      C:Species: Theobroma cacao (cacao)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: S22477; S22478; S18105; S22050
                                                                                                                                                                                                                                                                                                                                                                                       vicilin precursor - cacao
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A;Residues: 1-605 <CHL>
C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predicted <MAT>
      Query Match
Best Local Similarity
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A; Accession: S06398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
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A; Residues: 1-509 < CHL>
C; Superfamily: glycinin
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Best Local Similarity
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A;Status: not compared with conceptual translation
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38; Conser
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45.0%;
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53.8%;
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100.0%; <sub>F</sub>,
0;
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Pred.
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Pred. No. 8.4e-08;
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119; DB 2;
No. 2e-05;
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              Length 566;
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homeotic protein prospero - fruit fly (Drosophila melanogaster) (Species: Drosophila melanogaster) (C;Species: Drosophila melanogaster) (C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change C;Accession: S24548; JQ1397; A41089
submitted to the EMBL Data A; Reference number: S24548
                                                                                                                                    S24548
                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apolipoprotein A-IV - crab-eating macaque C;Species: Macaca fascicularis (crab-eating macaque) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 13-Aug-1999 C;Accession: S30195, S29565 R;Osada, J.; Pocovi, M.; Nicolosi, R.J.; Schaefer, E.J.; Ordovas, J.M. Biochim. Biophys. Acta 1172, 335-339, 1993 A;Title: Nucleotide sequences of the Macaca fascicularis apolipoprotein C-II
                                                                                                                                                                                                                                                                                                                                              A;Introns: 17/1; 59/2
C;Superfamily: apolipoprotein A-I
                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X68361; NID:g38050; PIDN:CAA48421.1; PID:g38051
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-429 <OSA>
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A;Accession: S30195
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submitted to the EMBL Data Library, January 1995
A;Description: An MDR transporter/serine protease gene
A;Reference number: Z18850
A;Accession: T18267
                                                                                                                                                                                                                                                                                   Query Match
Best Local
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A; Residues: 1-1905 <SHA>
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C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                       Matches
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          Library, February 1992
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42.5%;
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Pred. No. 0.
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A;Title: Highly conserved core domain and unique N R;Reference number: S10944; MUID:90326195 A;Accession: S10944 A;Molecule type: mRNA A;Residues: 1-91,96-339 <HOF> A;Cross-references: EMBL:X54993; NID:g37065; PIDN:CR;Kao, C.; Lieberman, P.; Schmidt, M.; Zhou, Q.; Pe Science 248, 1626, 1990
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C;Keywords: DNA binding; nucleus; transcr
F;717-734/Region: glutamine-rich
F;991-998/Region: nuclear location signal
F;1029-1049/Region: glutamine-rich
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Blochem. Blophys. Res. Commun. 182, 1326-1332, 1992
A;Title: Cloning of the Drosophila prospero gene and its expression in ganglion mot A; Reference number: JQ1397; MUID:92171948
A;Accession: JQ1397
A;Accession: JQ1397
A;Molecule type: mRNA
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A; Residues: 1-17,'N',19-186,'R',188-339
R; Hoffmann, A.; Sinn, E.; Yamamoto, T.;
Nature 346, 387-390, 1990
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A;Residues: 1-75,'GQDAERAVWPPDEAGPGRNEWPA',99-119,'NLALQFHVQVAAAAAITTALLPPIG',145-676,
A;Cross-references: GB:M81389; NID:g158183; PID:g158184
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A; Reference
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A; Residues: 1-339 < PET>
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C;Accession: A34830; A34831; S10944; I60128
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                     of the human TATA binding er: 160128
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54.8%;
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Q.; Pei, R.; Ber
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                                                            of a transcriptionally
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k, A.J.
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Query Match
Best Local Similarity
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R:Kuspa, A.; Lu, S.; Souza, G.M. submitted to the EMBL Data Library, Ja A; Description: Yaka, a protein kinase A; Reference number: Z18146
A; Accession: T14577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Hixson, J.E.; Kammerer, C.M.; Mott, G.E.; Britten, M.L.; Birnbaum, S.; Powers, J. Biol. Chem. 268, 15667-15673, 1993
A;Title: Babboon apolipoprotein A-TV. Identification of Lys76-->Glu that distingui A; Reference number: A47141; MUID:93340170
A;Status: preliminary
A;Status: preliminary
                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-1457 <KUS>
                                                                                                                                                                                                                                                                  protein kinase YakA (EC 2.7.1.-) - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apolipoprotein A-IV I isoform - baboon (fragment)
C;Species: Papio sp. (baboon)
C;Date: 16-Peb-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
A47141
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C; Superfamily: human transcription initiation:
C; Keywords: alternative splicing; DNA binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-186, 'R', 188-299, 'MIKPR', 300-339 < RES>A; Residues: 1-186, 'R', 188-299, 'MIKPR', 300-339 < RES>
  A;Gene: yakA
C;Keywords: ATP;
                                          A;Cross-references: EMBL:AF045453; NID:g2854116; PID:g2854117; PIDN:AAC02554.1C;Genetics:
                                                                                                                                                                                                                                                 C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: intestine A; Note: sequence extracted from NCBI backbone (NCBIN:136009, NCBIP:136010) C; Superfamily: apolipoprotein A-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: nucleic acid
A; Residues: 1-401 <HIX>
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19; Conser
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16; Conser
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  phosphoprotein; phosphotransferase;
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41.0%;
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Pred.
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serine/threonine-specific protei
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35.6%;

Score Pred.

NO;

DB 2; 0.49;

Length 1457

Matches

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A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin A;Note: important for cell type differentiation and fruiting body morphogenesis C;Superfamily: Dictyostelium cAMP-dependent protein kinase catalytic chain; protein kina F;126-223/Region: glutamine-rich F;297-312/Region: glutamine-rich F;297-312/Region: glutamine-rich F;334-590/Domain: protein kinase homology <KIN> F;342-550/Region: protein kinase ATP-binding motif F;365,384,459,461/Active site: Lys, Glu, Asp, Lys #status predicted F;464,468/Binding site: magnesium (Asn, Asp) #status predicted
                                                                                               οy
                                                            В
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C:Complex: heterodimer with regulatory chain; active catalytic chain is released when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Accession: JQ1150
R;Buerki, E.; Anjard, C.; Scholder, J.C.; Reymond, C.D.
Gene 102, 57-65, 1991
A;Title: Isolation of two genes encoding putative protein kinases regulated during Dicty A;Reference number: JQ1150; MUID:91323730
A;Accession: JQ1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein kinase (EC 2.7.1.37) cAMP-dependent, catalytic chain - slime mold (Dictyostelium
C:Species: Dictyostelium discoideum
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 24-Apr-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: PK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M38703C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-648 <BUE>
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A; Residues: 1-613 <BES>
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S27770
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13
                                                                                   1 PEDPORRYEECQQECRQQEERQQPQCQQRCLKRFEQEQQQ 40
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17; Conser
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37.5%;
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Pred. No. 0.4;
12; Mismatches
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Pred. No. 0
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0.39;
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C:Accession: T13675
R:Bolshakov, V.; Borkova, D.; Minana, B.; Kafatos, submitted to the EMBL Data Library, September 1998
submitted to the EMBL Data Library September 1998
                                                                                                                              C)Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jun-2000
A;Status: preliminary; translated A;Molecule type: DNA
                                                    A; Reference number: 217698
                                                                     A; Description: Sequencing
                                                                                                                                                                                                        RESULT
T13675
                                         A; Accession: T13675
                                                                                                                                                                    hypothetical protein EG0002.3 - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-758 <HUN>
A;Cross-references: GB:Z49705;
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references:
A;Map position: 13R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein YMR164c - yeast (Saccharomyces N;Alternate names: hypothetical protein YM8520.13c C:Species: Saccharomyces cerevisiae C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number:
A;Accession: S54522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, May 1995 A; Reference number: 854510\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: SGD: MSS11
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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 15
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A; Introns: 18/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: CESP: AC3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein AC3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Status: preliminary; translated from GB/EMBL/DDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: T18592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data A; Reference number: Z18995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: T
R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S.; Bowman, S.
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                                                                                                                                                                                                                                                                 PORRYEECQUECROQEERQQPQCQQRCLKRFEQEQQQ
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Conservative 10
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ce: clone AC3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain
                                                                                                                                                                                                                                                                                                                                                             34.28;
40.58;
                                                                  the distal X chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; EMBL:Z49700; NID:g825556; PIDN:CAA89800.1; PID:g825569
AB972
                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                        Score 77; DB 2;
Pred. No. 0.58;
13; Mismatches
           from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN:CAA94867.1; GSPDB:GN00023; CESP:AC3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 77; DB 2
Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        April
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                                                        of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                          Length 758;
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A;Residues: 1-1761 <- COLOR - COLOR -
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